



# By the Numbers

► by **Stephen Miller**, director of genetic research



## Improving the Angus carcass model

July 7, 2017, was a big day for Angus breeders, as results of the new genetic evaluation went live. This release was long anticipated and set a milestone as the first evaluation for a major U.S. beef breed to be based on single-step genomic evaluation methodology for all traits.

The switch to single-step methodology offered the opportunity to fit more complete models, and AGI staff took advantage of this to make some improvements to the carcass weight genetic evaluation model. These changes likely had a larger effect on carcass weight expected progeny differences (EPDs) than the switch to single-step methodology. Improvements to the carcass model, besides the obvious deployment of single-step methodology, included the addition of weaning weight and fat thickness traits (ultrasound and carcass), along with refreshed genetic parameters.

### Multi-trait model

The Association's genetic evaluation of carcass traits is based on a multiple-trait model, which is a powerful tool. The multi-trait methodology allows for important genetic correlations to be fit between traits. It is through these correlations that measured traits on a young bull, such as ultrasound ribeye area, can influence his carcass ribeye area EPD (REA).

In the case of REA, the model puts the right weighting on the scan record of the bull, as well as any relatives, including progeny that may be scanned along with carcass records. When a bull is young, his own scan record has a large influence on his EPD. As carcass information on progeny starts to come in, this new information takes precedence in influencing his EPD.

It is this seamless transition between data sources that is the elegance of the multi-trait model. By putting the correct emphasis on each source of information, the animal's EPD accuracy also reflects information content appropriately. Take REA as an example. Scan records can influence an animal's EPD; however, as a correlated trait, scan records can only take accuracy so far. To attain high levels of accuracy, actual carcass records on progeny are required.

Another capability of the multi-trait model is the ability to account for bias that can exist due to preselection.

Preselection bias is a challenge when animals are selected at weaning, which is common. It is typical that an entire calf crop would be weighed at weaning and lighter-weight animals culled at this stage. Consequently, those animals for which

yearling weight is measured are not an average sample of those at weaning. These animals are preselected and are, on average, higher-growth genetics than the average of the weaning group.

In the Angus growth evaluation, the multiple-trait model accounts for this preselection bias by evaluating all birth, weaning and yearling weights together. The new carcass evaluation model includes weaning weight, along with weights at a year of age (e.g., scan weight) together in the carcass evaluation model.

As live weight is a predictor of carcass weight, by better modeling the true genetic differences for live-weight genetics, the model is better accounting for correlated changes in carcass weight. The result is that carcass weight EPDs are now more reflective of genetic differences in growth.

### Adding fat to the model

Another powerful feature of the multi-

trait model is the ability to simultaneously fit the relationships among many different traits. In some cases a trait can be positively correlated with one trait, while being negatively correlated with another. These opposing relationships can be considered a push-pull effect; while one trait is trying to pull a trait up, another is pushing it down. In the end, there is an equilibrium where all opposing forces are equalized and the object, in this case the EPD, finds its resting place.

Opposing forces were added to the carcass weight model with the addition of fat thickness. Fat measured at a year of age is one indicator of maturity. When we analyzed the Angus data, we found that animals fatter at a year of age tended to have slightly lighter carcasses. This push downward on carcass weight by yearling ultrasound fat is offset by a positive relationship between carcass fat and carcass weight. As fat is left on the carcass, it contributes to carcass weight and this creates the observed positive relationship between carcass weight and carcass fat thickness.

These genetic correlations are low, so they are not having a large impact on how yearling bulls will rank for carcass weight, but they help better rank young animals through better modeling of all the pieces of information available.

Besides fitting more traits simultaneously, the carcass model has also been updated with a fresh estimation of genetic parameters. This refresh of the genetic parameters was not unique to the carcass model, but was done for all traits in all models. The most important genetic parameters (heritability and genetic correlations) related to understanding the new carcass model are illustrated in Table 1.

CONTINUED ON PAGE 64

**Table 1: Some important heritabilities and genetic correlations employed in the Angus multiple-trait carcass genetic evaluation**

	YW	U-FAT <sup>b</sup>	U-REA <sup>b</sup>	FAT	REA	CWT
WWT	0.87	—	—	—	—	—
YW	0.42 <sup>a</sup>	0.07	0.33	-0.07	0.35	0.75
U-FAT <sup>b</sup>		0.46 <sup>a</sup>	0	0.65	-0.35	-0.10
U-REA <sup>b</sup>			0.39 <sup>a</sup>	-0.1	0.65	0.28
FAT				0.33 <sup>a</sup>	-0.34	0.10
REA					0.32 <sup>a</sup>	0.46
CWT						0.44 <sup>a</sup>

<sup>a</sup>Heritabilities.

<sup>b</sup>Presented as ultrasound genetic parameters for bulls for illustration.

Since weaning weight and weight at a year, which is scan weight or yearling weight (YW), are very positively correlated (0.87), by fitting both traits for all weaned animals we better account for preselection bias.

All the ultrasound and carcass traits have a similar moderate heritability (0.32-0.46). Traits measured at a year of age have a strong correlation with carcass traits with YW correlated with carcass weight (0.75), and ultrasound correlated to carcass (0.65) for both FAT and REA. The correlation between ultrasound FAT and carcass weight is -0.10, while carcass weight and carcass fat is +0.1, which contributes to the modeling of differences in maturity patterns. As expected, bigger animals (live or carcass) have bigger REA, with a positive correlation (0.33) in the live animal, but also in the carcass (0.46). This interconnected matrix of relationships will all influence an animal's EPD.

### Enhancing tools for selection

The team at AGI continues to research ways to improve the predictability of the Angus genetic evaluation. These improvements to the carcass model represent one step forward and address some concerns breeders have expressed. Breeders had

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observed young animals with high YW EPD, but mediocre CW EPD. The changes implemented have created a more realistic relationship between carcass weight and growth EPDs.

When evaluating the improved accuracy of the new evaluation, one of the tests was to correlate the EPD from the new and old evaluations with EPDs generated by Larry Kuehn with the U.S. Meat Animal Research Center (USMARC) using data on progeny from 196 Angus bulls as an independent dataset. These improvements to the carcass model improved the accuracy of prediction for all the carcass traits. This independent validation by the USMARC that the new

evaluation is more accurate should give breeders confidence in the new evaluation using the improved model.

We're confident the national cattle evaluation provided by the American Angus Association was the best in the world prior to implementation of single step and the new carcass model, but we know we can't be complacent. New technology is constantly under development, and new techniques and added information offer opportunity to improve the genetic prediction tools in our toolbox.

Thoroughly analyzed internally and by peers, the changes we've implemented make the best better and lay a solid foundation for years to come as we continue to seek ways to enhance the Angus genetic evaluation.

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**Editor's Note:** "By the Numbers" is a column by Angus Genetics Inc. staff to share insights with Angus members about data collection and interpretation, the National Cattle Evaluation (NCE), genetic selection, and relevant technology and industry issues. If you have questions or would like to suggest a topic for a future column, contact Kelli Retallick, director of genetic service; Stephen Miller, director of genetic research, or Dan Moser, president, at 816-383-5100.